

## CLAIMS

1. A method for predicting biomolecular interactions comprising,  
inputting a training set comprising primary structure of biomolecules with known interactions into a trainable system,  
inputting a set of biomolecules with unknown interactions into the trainable system, and  
predicting interactions between members of the set of biomolecules with unknown interactions by analogy to the biomolecules in the training set using the trainable system.
2. The method of claim 1, wherein the interactions are homotypic.
3. The method of claim 1, wherein the interactions are heterotypic.
4. The method of claim 1, wherein the biomolecule is a protein.
5. The method of claim 1, wherein the biomolecule is a nucleic acid.
6. The method of claim 1, wherein the biomolecule is a bioactive agent.
7. A method for predicting whole proteome interactions comprising,  
inputting a training set comprising all known protein-protein interactions from a single organism into a trainable system,  
inputting a proteome of an organism with unknown interactions into the trainable system, and  
predicting interactions between members of the set of proteins with unknown interactions using the trainable system.
8. A trainable system for predicting biomolecular interactions comprising,  
a training set comprising primary structure of biomolecules with known interactions into a trainable system,

a set of biomolecules with unknown interactions into the trainable system, and  
a system for predicting interactions between members of the set of  
biomolecules with unknown interactions by analogy to the biomolecules in the  
training set.